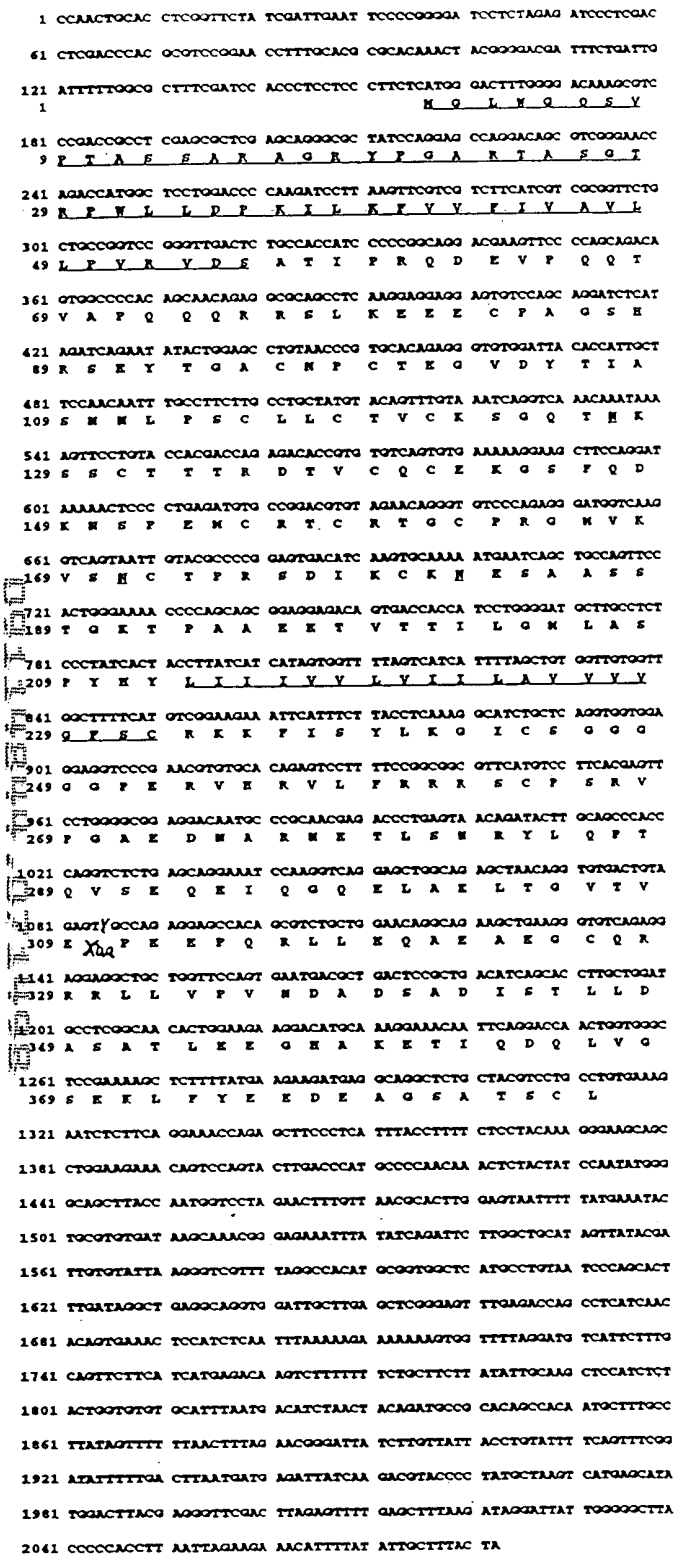

Fig. 1A

```
RTD     1 --MGLWGQSVPTASSARA--GRYPGARTASGTRPWLLDPKILKFVVFIVA
DR4    51 GRGALPTSMGQHGPSARARAGRAPGPRPAREASPRLRVHKTFKFV--VVG
DR5     1 --MEQRGQNAPAASGARKRHG--PGPREARGARPGLRVPKTLVLV--VVA
DcR1    1 --------------------------------MARIPKTLKFVVVIVA

RTD    47 VLLPVRVDSATIPRQDEVPQQTVAPQQQRRSLKEEECPAGSHRSEYTGAC
DR4    99 VLLQVVPSSAATIKLH---DQSIGTQQWEHSPLGELCPPGSHRSERPGAC
DR5    45 VLLLVSAESALITQQDLAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDC
DcR1   17 VLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGAC

                               CRD1
RTD    97 NPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSF
DR4   146 NRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTF
DR5    95 ISCKYGQDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQCEEGTF
DcR1   67 NPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEG

                   CRD2
RTD   147 QDKNSPEHCRTCRTGCPRGHVKVSNCTPRSDIKCKNESAASSTGKTPAAE
DR4   196 RNDNSAEHCRKCSTGCPRGHVKVKDCTPWSDIECVHKESGNGHNIW----
DR5   145 REEDSPEHCRKCRTGCPRGHVKVGDCTPWSDIECVHKESGIIIGVTVAA-
DcR1  117 RNENSPEHCRKCSR-CPSGEVQVSNCTSWDDIQCVEEFGANAT------
```

Fig. 1B

```
RTD   233 RKKFISYLKGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSN
DR4   269 -GGDPKCMDRVCFWRLG---------------LLRGPGAEDNAHNEILSN
DR5   209 --KVLPYLKGICSGGGGDPERVDR--------SSQRPGAEDNVLNEIVSI

RTD   283 RYLQPTQVSEQEIQGQELAELTGVTVESPEEPQRLLEQAEAEGCQRRRLL
DR4   303 ADSLSTFVSEQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRLL
DR5   250 --LQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLL

                  ---------------------- DD ---------------------
RTD   333 VPVNDAD-------------------------------------------
DR4   353 VPANGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTA
DR5   298 VPANEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAA

          ------------------------------------------------
RTD   340 -------------------SADISTLLDASATLEEGMAKETIQDQLVGSE
DR4   403 GPGDALYAMLMKWVNKTGRNASIMTLLDALERMEERMAKEKIQDLLVDSG
DR5   348 GHRDTLYTMLIKWVNKTGRDASVMTLLDALETLGERLAKQKIEDHLLSSG

RTD   371 KLFYEEDEAGSATSCL
DR4   453 KFIYLEDGTGSAVSLE
DR5   398 KFMYLEGNADSALS
```

Fig. 1C

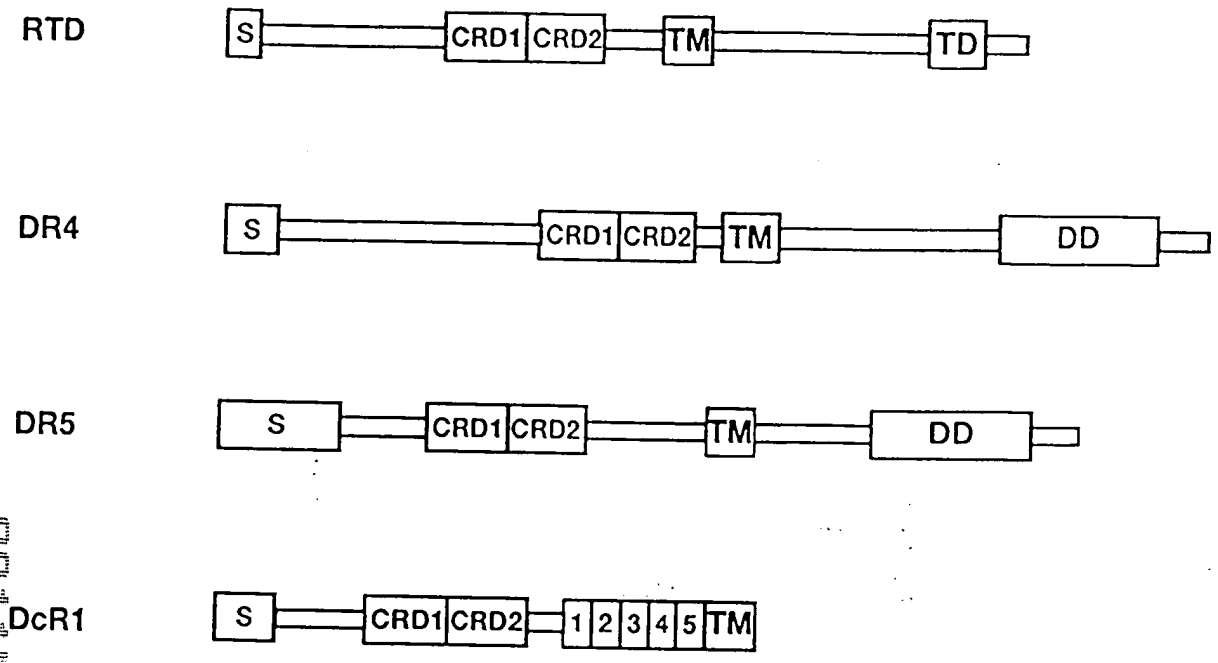
RTD
S
CRD1
CRD2
TM
TD
DR4
S
CRD1
CRD2
TM
DD
DR5
S
CRD1
CRD2
TM
DD
DcR1
S
CRD1
CRD2
1
2
3
4
5
TM

Fig. 1D

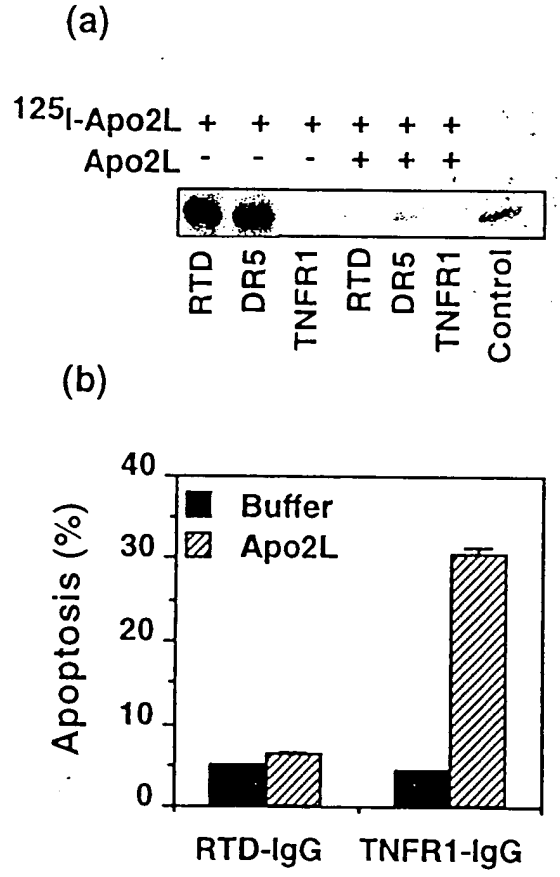
(a)
125I-Apo2L + + + + + +
Apo2L - - - + + +
RTD
DR5
TNFR1
RTD
DR5
TNFR1
Control
(b)
Apoptosis (%)
40
30
20
10
0
Buffer
Apo2L
RTD-IgG
TNFR1-IgG

Fig. 2

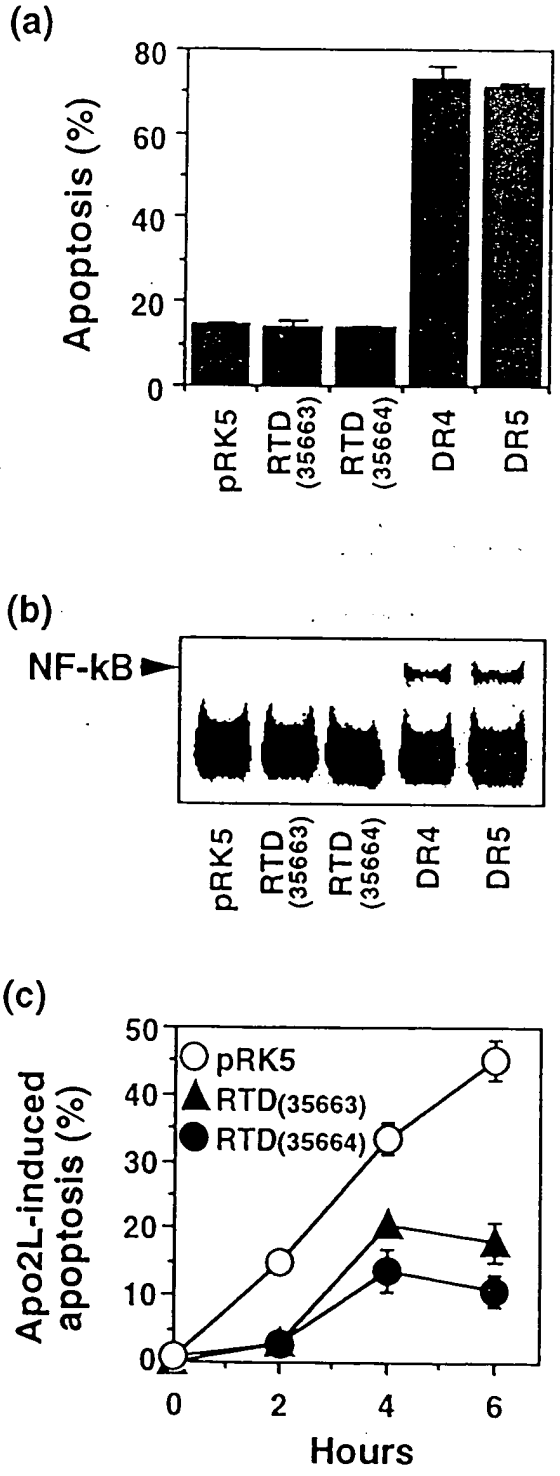

Fig. 3

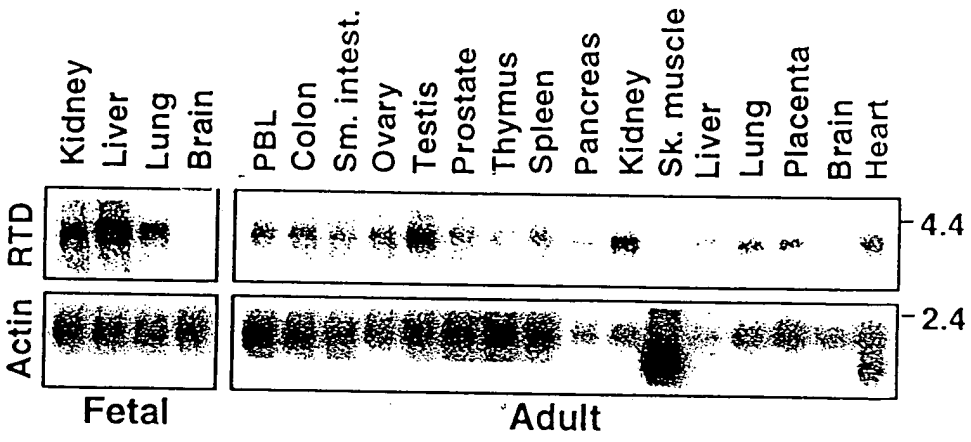
Kidney
Liver
Lung
Brain
PBL
Colon
Sm. intest.
Ovary
Testis
Prostate
Thymus
Spleen
Pancreas
Kidney
Sk. muscle
Liver
Lung
Placenta
Brain
Heart
RTD
Actin
4.4
2.4
Fetal
Adult

Fig. 4